FIGURE 1A

	TTGAATGCTAGGTTCTGATTCCCTCTTCCACCCTCTGCCTCTTTAGCCTCTATC	09
61	<u>ATG</u> TGGAACAGCTCTGACGCCAACTTCTCCTGCTACCATGAGTCTGTGCTGGGCTATCGT	120
121	TATGTTGCAGTTAGCTGGGGGGGGGGGGGGCTGTGACAGGCACCGTGGGCAATGTGCTC	180
181	ACCCTACTGGCCTTGGCCATCCAGCCCCAAGCTCCGTACCCGATTCAACCTGCTCATAGCC	240
241	AACCTCACACTGGCTGATCTCCTCTACTGCACGCTCCTTCAGCCCTTCTCTGTGGACACC	300
301	TACCTCCACCTGCACTGGCGCACCGGTGCCACCTTCTGCAGGGTATTTGGGGCTCCTCTT	360
361	TTTGCCTCCAATTCTGTCTCCATCCTGACCCTCTGCCTCATCGCACTGGGACGCTACCTC	420
421	CTCATTGCCCACCCTAAGCTTTTTCCCCAAGTTTTCAGTGCCAAGGGGATAGTGCTGGCA	480
481	CTGGTGAGCACCTGGGTTGTGGGCGTGGCCAGCTTTGCTCCCCCTCTGGCCTATTATATC	540
541	CTGGTACCTGTAGTCTGCACCTGCAGCTTTGACCGCCATCCGAGGCCGGCC	009
601	ATCCICATGGGCATCTACTTTGTGCTTGGGCTCAGCAGTGTTGGCATCTTCTATTGCCTC	099
661	ATCCACCGCCAGGTCAAACGAGCAGCACAGGCACTGGACCAATACAAGTTGCGACAGGCA	720
721	AGCATCCACTCCAACCATGTGGCCAGGACTGATGAGGCCATGCCTGGTCGTTTCCAGGAG	780

FIGURE 1B

	CCTAGTCACCAGAATTCAGGACTGTCTCCTCCAGGACCAAAGTGGCAGGTA 1311	1261
1260	TATGGCTCCATTTTAAAAAGAGGGCCCCGGAGTTTCCATAGGCTCCAT <u>TAG</u> AACTGTGAC	1201
1200	CTCAATGGTTGCATCAACCCTGTGCTCTATGCAGCCATGAACCGCCAATTCCGCCAAGCA	1141
1140	CTGGATGCCAGAGTCCCCCGGGTGGTCCACATGCTTGCTGCCAACCTCACCTGG	1081
1080	TGTTTTGCTGTGTTCCTCTGCTTTGCCCTGAGCTACATCCCCTTCTTGCTGCTCAACATT	1021
1020	ATTAAAGGAGCCAGAAGAGCTCCGGATTCTTCATCGGAATTTTGGGAAGGTGACTCGAATG	961
096	AAGAGAGCTAAGCCAGAGAGAAAAGCCCTCCAGAAGCATCTGCCAAAGCCAGCC	901
006	GCTGCCACCCAGACCCTGGAAGGGGACTCATCAGAAGTGGGAGACCAGATCAACAGC	841
840	CTGGACAGCAGGTTAGCATCAGGAGGACCCAGTGAGGGGGATTTCATCTGAGCCAGTCAGT	781

FIGURE 2A

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FIGURE 2B

160	180	200	220	240	260	280	300	320
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141	161	181	201	221	241	261	281	301

FIGURE 2C

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321	341	361	381



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